

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: November 7, 2002, 10:02:29 ; Search time 8.04545 Seconds  
(without alignments)  
3060.813 Million cell updates/sec

Title: US-09-125-005-6

Perfect score: 3384

Sequence: 1 MAQSTATSPDGGTTFEHLWS.....PDCKARKOPIKEEFTAEIHT 636

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score  | Query Match | Length | DB ID       | Description         |
|------------|--------|-------------|--------|-------------|---------------------|
| 1          | 3384   | 100.0       | 636    | 1 P73_HUMAN | O15350 homo sapien  |
| 2          | 3304.5 | 97.7        | 636    | 1 P73_CERAE | O9XSK8 cercoptithec |
| 3          | 851.5  | 25.2        | 396    | 1 P53_ONCMY | P25035 oncorhynchu  |
| 4          | 821    | 24.3        | 369    | 1 P53_BABU  | O9W678 barbus barb  |
| 5          | 801.5  | 23.7        | 373    | 1 P53_BRARE | P79734 brachydiano  |
| 6          | 790.5  | 23.4        | 386    | 1 P53_FIG   | Q9TUB2 sus scrofa   |
| 7          | 789.5  | 23.0        | 381    | 1 P53_ICTPU | O93379 ictalurus p  |
| 8          | 778.5  | 23.0        | 381    | 1 P53_CANFA | Q29537 canis famil  |
| 9          | 778    | 22.9        | 367    | 1 P53_CHICK | P10360 gallus gall  |
| 10         | 776    | 22.9        | 386    | 1 P53_FELCA | P41685 felis silve  |
| 11         | 760.5  | 22.5        | 386    | 1 P53_BOVIN | Q29628 bos taurus   |
| 12         | 755.5  | 22.3        | 382    | 1 P53_SHEEP | P51684 ovis aries   |
| 13         | 752    | 22.2        | 351    | 1 P53_ORYLA | P79820 oryzias lat  |
| 14         | 750.5  | 22.2        | 391    | 1 P53_CAVPO | Q9WUR6 cavia porce  |
| 15         | 749    | 22.1        | 396    | 1 P53_MESAU | Q00366 mesocricetu  |
| 16         | 745.5  | 22.0        | 393    | 1 P53_CRIGR | O09185 cricetulus   |
| 17         | 741    | 21.9        | 363    | 1 P53_XENLA | P07193 xenopus lae  |
| 18         | 739.5  | 21.9        | 393    | 1 P53_TUPGB | Q9TAL1 tupiaia glis |
| 19         | 736.5  | 21.8        | 391    | 1 P53_MARMO | O36006 marmota mon  |
| 20         | 735.5  | 21.7        | 391    | 1 P53_RAT   | P10361 rattus norv  |
| 21         | 731.5  | 21.6        | 367    | 1 P53_TETMU | O9W679 tetraodon m  |
| 22         | 725.5  | 21.4        | 393    | 1 P53_MACMU | P56424 macaca mula  |
| 23         | 724.5  | 21.4        | 391    | 1 P53_RABIT | O95330 coryctolagus |
| 24         | 724.5  | 21.4        | 393    | 1 P53_HUMAN | P04637 homo sapien  |
| 25         | 723.5  | 21.4        | 393    | 1 P53_MACFA | P56423 macaca fasc  |
| 26         | 718.5  | 21.2        | 393    | 1 P53_CERAE | P13481 cercoptithec |
| 27         | 711.5  | 21.0        | 390    | 1 P53_MOUSE | P02340 mus musculu  |
| 28         | 695    | 20.5        | 366    | 1 P53_PLAFE | O12946 platichthys  |
| 29         | 691.5  | 20.4        | 280    | 1 P53_HORSE | P79892 equus cabal  |
| 30         | 686.5  | 20.3        | 314    | 1 P53_SPERE | O64662 spermophilu  |
| 31         | 686    | 20.3        | 342    | 1 P53_XIPHE | O57538 xiphophorus  |
| 32         | 686    | 20.3        | 342    | 1 P53_XIPMA | Q92143 xiphophorus  |
| 33         | 600.5  | 17.7        | 207    | 1 P53_EQUAS | Q29480 equus asinu  |

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|----|-------|-----|------|---|------------|--------------------|
| 34 | 133   | 3.9 | 1273 | 1 | WEB1_YEAST | P38968 saccharomyc |
| 35 | 131.5 | 3.9 | 2459 | 1 | MAPB_RAT   | P15205 rattus norv |
| 36 | 129   | 3.8 | 306  | 1 | EXTN_DAUCA | P06599 daucus caro |
| 37 | 127.5 | 3.8 | 784  | 1 | SP4_HUMAN  | Q02446 homo sapien |
| 38 | 126.5 | 3.7 | 1386 | 1 | ZAP3_MOUSE | Q9R017 mus musculu |
| 39 | 126   | 3.7 | 817  | 1 | VRP1_YEAST | P37370 saccharomyc |
| 40 | 126   | 3.7 | 1902 | 1 | SMF1_HUMAN | O14497 homo sapien |
| 41 | 124.5 | 3.7 | 3358 | 1 | PGCV_MOUSE | Q62059 mus musculu |
| 42 | 124   | 3.7 | 1051 | 1 | ULK1_MOUSE | O70405 mus musculu |
| 43 | 124   | 3.7 | 1972 | 1 | P531_HUMAN | O12888 homo sapien |
| 44 | 123.5 | 3.6 | 1618 | 1 | NES1_HUMAN | P48881 homo sapien |
| 45 | 123   | 3.6 | 1227 | 1 | LAF4_HUMAN | P51826 homo sapien |

ALIGNMENTS

RESULT 1  
P73\_HUMAN  
ID P73\_HUMAN STANDARD; PRT; 636 AA.  
AC O15350; O15351; Q9NTK8;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Tumor protein p73 (p53-like transcription factor) (p53-related protein).  
GN TP73 OR P73.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).  
RC TISSUE=Colon;  
RX MEDLINE=974333090; PubMed=9288759;  
RA Kaghad M., Bonnet H., Yang A., Creancier L., Biscan J.-C., Valent A., Minty A., Chalon P., Lelias J.-M., Dumont X., Ferrara P., McKeon F., Caput D.;  
RT "Monoclonally expressed gene related to p53 at 1p36, a region frequently deleted in neuroblastoma and other human cancers.";  
Cell 90:809-819(1997).

RL [2]  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).  
RX MEDLINE=9289209; PubMed=1032363;  
RA Yoshikawa H., Nagashima M., Khan M.A., McMenamin M.G., Hagiwara K., Harris C.C.;  
RT "Mutational analysis of p73 and p53 in human cancer cell lines.";  
Oncogene 18:3415-3421(1999).

RL [3]  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).  
RX MEDLINE=98389621; PubMed=9721206;  
RA Mai M., Huang H., Reed C., Qian C., Smith J.S., Alderete B., Jenkins R., Smith D.I., Liu W.;  
RT "Genomic organization and mutation analysis of p73 in oligodendrogliomas with chromosome 1 p-arm deletions.";  
Genomics 51:359-363(1998).

RL [4]  
RN [4]  
RP SEQUENCE FROM N.A. (ISOFORMS GAMMA AND DELTA).  
RC TISSUE=Neuroblastoma;  
RX MEDLINE=99021697; PubMed=9802988;  
RA De Laurenzi V., Costanzo A., Barcaroli D., Terrinoni A., Falco M., Annicchiarico-Petruzzelli M., Leviero M., Melino G.;  
RT "Two new p73 splice variants, gamma and delta, with different transcriptional activity.";  
J. Exp. Med. 188:1763-1768(1998).

RL [5]  
RN [5]  
RP SEQUENCE FROM N.A. (ISOFORMS EPSILON AND ZETA).  
RC TISSUE=Lymphocytes, Breast cancer, Hepatoma, and Skin;  
RX MEDLINE=99310938; PubMed=10381648;  
RA De Laurenzi V., Catani M.V., Terrinoni A., Corazzari M., Melino G., Costanzo A., Leviero M., Knight R.A.;  
RT "Additional complexity in p73: induction by mitogens in lymphoid cells and identification of two new splicing variants epsilon and zeta.";

2/3/97/7/3/98

Cell Death Differ. 6:389-2001-10997  
 [6] SEQUENCE FROM N.A. (ISOFORM KAPPA).  
 RA Thomas D.;  
 RN Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.  
 [7]  
 RP PHOSPHORYLATION (ISOFORMS ALPHA AND BETA).  
 RA MEDLINE-99318135; PubMed-10391251;  
 RA Yuan Z.-M., Shioya H., Ishiko T., Sun X., Gu J., Huang Y., Lu H.,  
 RA Kharbanda S., Weichselbaum R., Kufe D.;  
 RT "p73 is regulated by tyrosine kinase c-Abl in the apoptotic response  
 RT to DNA damage.";  
 RL Nature 399:814-817(1999).  
 [8]  
 RP ERRATUM.  
 RA Yuan Z.-M., Shioya H., Ishiko T., Sun X., Gu J., Huang Y., Lu H.,  
 RA Kharbanda S., Weichselbaum R., Kufe D.;  
 RL Nature 400:792-792(1999).  
 [9]  
 RP FUNCTION.  
 RA MEDLINE-99217940; PubMed-10203277;  
 RA Kaelin W.G. Jr.;  
 RT "The emerging p53 gene family.";  
 RL J. Natl. Cancer Inst. 91:594-598(1999).  
 [10]  
 RP STRUCTURE BY NMR OF 439-506.  
 RX MEDLINE-99380160; PubMed-1049409;  
 RA Chi S.W., Ayed A., Arrowsmith C.H.;  
 RT "Solution structure of a conserved C-terminal domain of p73 with  
 RT structural homology to the SAM domain.";  
 RL EMBO J. 18:4438-4445(1999).  
 CC -!- FUNCTION: PARTICIPATES IN THE APOPTOTIC RESPONSE TO DNA DAMAGE.  
 CC WHEN OVERPRODUCED, ACTIVATES TRANSCRIPTION FROM P53-RESPONSIVE  
 CC PROMOTERS AND INDUCES APOPTOSIS. MAY BE A TUMOR SUPPRESSOR  
 CC PROTEIN.  
 CC -!- SUBUNIT: THE C-TERMINAL OLIGOMERIZATION DOMAIN BINDS TO THE ABL  
 CC TYROSINE KINASE SH3 DOMAIN. ISOFORM BETA INTERACTS HOMOTYPICALLY  
 CC AND WITH P53, WHEREAS ISOFORM ALPHA DOES NOT. ISOFORM GAMMA  
 CC INTERACTS HOMOTYPICALLY AND WITH ALL P73 ISOFORMS. ISOFORM DELTA  
 CC INTERACTS WITH ISOFORM GAMMA, ALPHA, AND HOMOTYPICALLY.  
 CC -!- SUBCELLULAR LOCATION: Nuclear.  
 CC -!- ALTERNATIVE PRODUCTS: 7 ISOFORMS; ALPHA (SHOWN HERE), BETA, GAMMA,  
 CC DELTA, EPSILON, ZETA AND KAPPA; ARE PRODUCED BY ALTERNATIVE  
 CC SPLICING. THE SPLICING OF EXON 11 IN GAMMA AND EPSILON ISOFORMS  
 CC RESULTS IN A FRAMESHIFT FROM THE ORIGINAL READING FRAME. THE  
 CC SPLICING OF EXON 13 IN EPSILON ISOFORM REVERTS THE READING FRAME  
 CC TO THE ALPHA ISOFORM.  
 CC -!- TISSUE SPECIFICITY: BRAIN, KIDNEY, PLACENTA, COLON, HEART, LIVER,  
 CC SPLEEN, SKELETAL MUSCLE, PROSTATE, THYMUS AND PANCREAS.  
 CC -!- INDUCTION: NOT INDUCED BY DNA DAMAGE.  
 CC -!- DOMAIN: POSSESSES AN ACIDIC TRANSACTIVATION DOMAIN, A CENTRAL DNA  
 CC BINDING DOMAIN AND A C-TERMINAL OLIGOMERIZATION DOMAIN THAT BINDS  
 CC TO THE ABL TYROSINE KINASE SH3 DOMAIN.  
 CC -!- DISEASE: MAPS TO A CHROMOSOME REGION FREQUENTLY MUTATED IN DIVERSE  
 CC CELL LINES OF HUMAN CANCER. APPEARS NOT TO BE FREQUENTLY MUTATED  
 CC IN HUMAN CANCERS, IN CONTRAST TO P53. HEMIZYGOSITY IS OBSERVED IN  
 CC NEUROBLASTOMA AND OLIGODENDROGLIOMA.  
 CC -!- SIMILARITY: BELONGS TO THE P53 FAMILY.  
 CC  
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| QY                        | 61   | VMAQFNLLS  | TMDQMSRAASAPYTPEHAASVPTHTSPAQSSFTFTMTSPAPVIPESNTD  | 120     |  |  |  |  |  |
| DB                        |  |  |  |         |  |  |  |  |  |
| DB                        | 61   | VMAQFNLLS  | TMDQMSRAASAPYTPEHAASVPTHTSPAQSSFTFTMTSPAPVIPESNTD  | 120     |  |  |  |  |  |
| QY                        | 121  | YGPPIHFEVT   | FQQGSTAKSATWITYSPLLKKLYCQIAKTCPIQIKVSTPPPGTAIRAMPV | 180     |  |  |  |  |  |
| DB                        |  |  |  |         |  |  |  |  |  |
| DB                        | 121  | YGPPIHFEVT   | FQQGSTAKSATWITYSPLLKKLYCQIAKTCPIQIKVSTPPPGTAIRAMPV | 180     |  |  |  |  |  |
| QY                        | 181  | YKKAHEHVDV   | VVKRCPNHELGRDFNEGQSAPASHLIRVEGNLSQYVDDPVTGQSVVVYP  | 240     |  |  |  |  |  |
| DB                        |  |  |  |         |  |  |  |  |  |
| DB                        | 181  | YKKAHEHVDV   | VVKRCPNHELGRDFNEGQSAPASHLIRVEGNLSQYVDDPVTGQSVVVYP  | 240     |  |  |  |  |  |
| QY                        | 241  | EPPQVGTEFTT  | LNFMCNNSCVGGNNRRPILIIITLEWRDGQVLGRRSFEGRICACPCR    | 300     |  |  |  |  |  |
| DB                        |  |  |  |         |  |  |  |  |  |
| DB                        | 241  | EPPQVGTEFTT  | LNFMCNNSCVGGNNRRPILIIITLEWRDGQVLGRRSFEGRICACPCR    | 300     |  |  |  |  |  |
| QY                        | 301  | DRKADEDHRYEQQA   | NLESSAKGAASKRAFQSPPAVPALGAGVKKRHHGDETYTLQVR        | 360     |  |  |  |  |  |
| DB                        |  |  |  |         |  |  |  |  |  |
| DB                        | 301  | DRKADEDHRYEQQA   | NLESSAKGAASKRAFQSPPAVPALGAGVKKRHHGDETYTLQVR        | 360     |  |  |  |  |  |
| QY                        | 361  | GRENFEILMKLESLE  | MELVPOPLVDSYRQOQLLPRLSHQPPSGPVLSPMNKVHG            | 420     |  |  |  |  |  |
| DB                        |  |  |  |         |  |  |  |  |  |
| DB                        | 361  | GRENFEILMKLESLE  | MELVPOPLVDSYRQOQLLPRLSHQPPSGPVLSPMNKVHG            | 420     |  |  |  |  |  |
| QY                        | 421  | MNKLPSVNOLVQP  | PHISSAATNLGPGVGMNNHGHAVPANGEMSSSHSAOSMWVSGSH       | 480     |  |  |  |  |  |
| DB                        |  |  |  |         |  |  |  |  |  |
| DB                        | 421  | MNKLPSVNOLVQP  | PHISSAATNLGPGVGMNNHGHAVPANGEMSSSHSAOSMWVSGSH       | 480     |  |  |  |  |  |
| QY                        | 481  | CTPPPPYHADPSLV   | SFYTGIGCPNCIEYFTSOGLSIYHLQNLTIEDLGALKIPEQYRMT      | 540     |  |  |  |  |  |
| DB                        |  |  |  |         |  |  |  |  |  |
| DB                        | 481  | CTPPPPYHADPSLV   | SFYTGIGCPNCIEYFTSOGLSIYHLQNLTIEDLGALKIPEQYRMT      | 540     |  |  |  |  |  |
| QY                        | 541  | IWRGLDLKQCHDY  | STAQILLRSSNAATISIGSGELORQRVMEAVFRVHRHTTIPNRG       | 600     |  |  |  |  |  |
| DB                        |  |  |  |         |  |  |  |  |  |
| DB                        | 541  | IWRGLDLKQCHDY  | STAQILLRSSNAATISIGSGELORQRVMEAVFRVHRHTTIPNRG       | 600     |  |  |  |  |  |
| QY                        | 601  | GPGGPDWEADFG   | DLPCKARKAPIKEEFTAEIH                               | 636     |  |  |  |  |  |
| DB                        |  |  |  |         |  |  |  |  |  |
| DB                        | 601  | GPGGPDWEADFG   | DLPCKARKAPIKEEFTAEIH                               | 636     |  |  |  |  |  |
| <br>RESULT 2<br>P73.CERAE |  |  |  |         |  |  |  |  |  |
| ID                        | P73.CERAE  | STANDARD;  | PRT:   | 637 AA. |  |  |  |  |  |
| AC                        | O9XK8;   | Q9TS09;  |  |         |  |  |  |  |  |
| DT                        | 16-OCT-2001  | (Rel. 40,  | Created)   |         |  |  |  |  |  |
| DT                        | 16-OCT-2001  | (Rel. 40,  | Last sequence update)                              |         |  |  |  |  |  |
| DE                        | 16-OCT-2001  | (Rel. 40,  | Last annotation update)                            |         |  |  |  |  |  |
| DE                        | tumor protein p73 (p53-like transcription factor) (p53-related protein). |  |  |         |  |  |  |  |  |
| DN                        | TP73 OR P73.   |  |  |         |  |  |  |  |  |
| OC                        | Cercopithecus aethiops   | (Green monkey) (Grivet).   |  |         |  |  |  |  |  |
| OC                        | Eukaryota; Metazoa;  | Chordata; Craniata; Vertebrata; Euteleostomi;  |  |         |  |  |  |  |  |
| OC                        | Mammalia; Eutheria;  | Primates; Catarrhini; Cercopithecoidea;  |  |         |  |  |  |  |  |
| OC                        | Cercopithecinae;   | Cercopithecus.   |  |         |  |  |  |  |  |
| OX                        | NCBI_TaxID=9534;   |  |  |         |  |  |  |  |  |
| RN                        | [1]  |  |  |         |  |  |  |  |  |
| RP                        | SEQUENCE FROM N.A.   |  |  |         |  |  |  |  |  |
| RC                        | TISSUE=Kidney;   |  |  |         |  |  |  |  |  |
| RA                        | Caput D.;  |  |  |         |  |  |  |  |  |
| RL                        | Submitted (Feb-1997) to the EMBL/GenBank/DBJ databases.                  |  |  |         |  |  |  |  |  |
| CC                        | -1-  | FUNCTION: PARTICIPATES IN THE APOPTOTIC RESPONSE TO DNA DAMAGE.  |  |         |  |  |  |  |  |
| CC                        | CC   | WHEN OVERPRODUCED, ACTIVATES TRANSCRIPTION FROM P53-RESPONSIVE PROMOTERS AND INDUCES APOPTOSIS. MAY BE A TUMOR SUPPRESSOR PROTEIN (BY SIMILARITY).                             |  |         |  |  |  |  |  |
| CC                        | -1-  | SUBUNIT: THE C-TERMINAL OLIGOMERIZATION DOMAIN BINDS TO THE ABL TYROSINE KINASE SH3 DOMAIN. ISOFORM BETA INTERACTS HOMOTYPICALLY AND WITH P53, WHEREAS ISOFORM ALPHA DOES NOT. |  |         |  |  |  |  |  |
| CC                        | -1-  | SUBCELLULAR LOCATION: Nuclear.   |  |         |  |  |  |  |  |
| CC                        | -1-  | ALTERNATIVE PRODUCTS: 2 ISOFORMS; ALPHA (SHOWN HERE) AND BETA;   |  |         |  |  |  |  |  |
| CC                        | -1-  | DOMAIN: POSSESSES AN ACIDIC TRANSACTIVATION DOMAIN, A CENTRAL DNA  |  |         |  |  |  |  |  |

[illegible]

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FT DOMAIN 1 28 TRANSCRIPTION ACTIVATION (ACIDIC).
FT DNA_BIND 66 BY SIMILARITY.
FT DOMAIN 298 OLIGOMERIZATION.
FT DOMAIN 329 BASIC (REPRESSION OF DNA-BINDING).
FT DOMAIN 342 BASIC (REPRESSION OF DNA-BINDING).
FT DOMAIN 276 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT MOD_RES 368 PHOSPHORYLATION (BY SIMILARITY).
SQ SEQUENCE 369 AA; 41233 MW; 0BE2CF2CEA74C304 CRC64;

Query Match 24.3%; Score 821; DB 1; Length 369;
Best Local Similarity 54.0%; Pred. No. 6.3e-48;
Matches 169; Conservative 49; Mismatches 83; Indels 12; Gaps 7;

QY 83 SPYTPHAAASVPTSPYAPQSPSTEDTMSAPVPSNTDYPGPHFHEFTVFOOSSTAKSATW 142
DB 35 SFEDNFDNVTQSP--QPS-----TSPTASVPVAIDYGEHGFKLGFQSGTAKSVTC 88

QY 143 TYSPLKLYCQIAKTCPIQIKVSTPTPPGTAIRAMPVYKAEHVDVVKRCNHELGRD 202
DB 89 TVSSDLNLFECOLAKTCPQVMVNVAPPQGSVIRATAIYKKSEHVAEVRRCPPHERTPD 148

QY 203 FNEGOSAPASHLIRVEGNLSQYVDDPVTGROSVVVEYEPQVGTETTTLYNFMNCSSC 262
DB 149 -GDG-LAPAAHLIRVEGNLSQYVDDPVTGROSVVVEYEPQVGTETTTLYNFMNCSSC 206

QY 263 VGMNRRPILITILEMRDQVLGRSFEGRICACPGDRKADDEHYEQOALNESSAKN 322
DB 207 MCGMNRRLITILITLEDHGGQLGRSFEVRVACPGDRKTESNFKDQE-TKTLDKI 265

QY 323 GAASRAFP-KOSPAPVAPALGAGVKKRRHG--DETYIYLVQVGRNFELMKLESLELME 379
DB 266 PSANKRSTKDTSTSPVPEGSKKALSGSSDEIYTLQVRGKERYEMLKINDSLELSD 325

QY 380 LVPQPLVDSYRQO 392
DB 326 VYPPSEMDRYRQK 338

RESULT 5
P53_BRARE
ID P53_BRARE STANDARD; PRT; 373 AA.
AC P79734;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Cellular tumor antigen p53 (Tumor suppressor p53).
GN TP53.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97344388; PubMed=9200835;
RA Cheng R., Ford B.L., O'Neal P.E., Mathews C.Z., Bradford C.S.,
RA Thongtan T., Barnes D.W., Hendricks J.D., Bailey G.S.;
RA "Zebrafish (Danio rerio) p53 tumor suppressor gene: cDNA sequence and
RT expression during embryogenesis.";
RL Mol. Mar. Biol. Biotechnol. 6:88-97(1997).
CC -1- GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL
CC CIRCUMSTANCES OR CELL TYPE, BUT BOTH ACTIVITIES ARE INVOLVED IN
CC TUMOR SUPPRESSION. ACTS IN CELL CYCLE REGULATION, IS A TRANS-
CC ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION BY
CC CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF THE
CC ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES.
CC APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF
CC BAX AND BCL-2 ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2
CC EXPRESSION (BY SIMILARITY).
CC -1- SUBUNIT: BINDS DNA AS AN HOMOTETRAMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
CC -----

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CC -----
CC EMBL; U60804; ABA0617.1;
CC HSP; P04637; ITUP.
CC ZFIN; ZDB-GENE-990415-270; tp53.
CC InterPro; IPR002117; P53.
CC Pfam; PF00870; P53; 1.
CC PRINTS; PR00386; P53SUPPRESSOR.
CC PRODOM; PD002681; P53; 1.
CC PROSITE; PS00348; P53; 1.
CC Anti-oncogene; DNA-binding; Transcription regulation; Activator;
CC Nuclear protein; Phosphorylation; Apoptosis.
CC FT DOMAIN 1 31 TRANSCRIPTION ACTIVATION (ACIDIC).
CC BY SIMILARITY.
CC FT DNA_BIND 70 260 OLIGOMERIZATION.
CC FT DOMAIN 301 332 BASIC (REPRESSION OF DNA-BINDING).
CC FT DOMAIN 345 366 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
CC FT DOMAIN 280 296 PHOSPHORYLATION (BY SIMILARITY).
CC FT MOD_RES 372 372 PHOSPHORYLATION (BY SIMILARITY).
CC SQ SEQUENCE 373 AA; 41899 MW; AC7AB724FA6B61FF CRC64;

Query Match 23.7%; Score 801.5; DB 1; Length 373;
Best Local Similarity 51.0%; Pred. No. 1.3e-46;
Matches 158; Conservative 50; Mismatches 91; Indels 11; Gaps 5;

QY 85 YTPHAAASVPTSPYAPQSPSTEDTMSAPVPSNTDYPGPHFHEFTVFOOSSTAKSATW 144
DB 41 FDPNFFENVEEQP--QPS-----TLPSTVPTSDTDPGDFRFPQSGTAKSVTCY 94

QY 145 SPLKLYCQIAKTCPIQIKVSTPTPPGTAIRAMPVYKAEHVDVVKRCNHELGRDN 204
DB 95 SPDLNLFECOLAKTCPQVMVNVAPPQGSVIRATAIYKKSEHVAEVRRCPPHHE--RTPD 152

QY 205 EQSAPASHLIRVEGNLSQYVDDPVTGROSVVVEYEPQVGTETTTLYNFMNCSSCVG 264
DB 153 GDLAPAGHLIRVEGNLSQYVDDPVTGROSVVVEYEPQVGTETTTLYNFMNCSSCVG 212

QY 265 GMRPILITILEMRDQVLGRSFEGRICACPGDRKADDEHYEQOALNESSAKNGA 324
DB 213 GMRPILITILEMRDQVLGRSFEGRICACPGDRKADDEHYEQOALNESSAKNGA 271

QY 325 ASKRAFQSPVAPVAPALGAGVKKRR--HGDETYIYLVQVGRNFELMKLESLELME 382
DB 272 GPKRSLVRESSATLRPEGSKKAGSSSDEIYTLQVRGKERYEILKINDSLELSDVVP 331

QY 383 QPLVDSYRQO 392
DB 332 ASDAEKRYRQK 341

RESULT 6
P53_PIG
ID P53_PIG STANDARD; PRT; 386 AA.
AC Q9TUB2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cellular tumor antigen p53 (tumor suppressor p53).
GN TP53 OR P53.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Burr P.D., Argyle D.J., Reid S.W.J., Nasir L.;
RT "Nucleotide sequence of the pig p53 tumor suppressor cDNA.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
CC -----
```







[illegible]



SEQUENCE FROM N.A.  
SPECIES-B.indicus; STRAIN-BORAN; TISSUE-Blood;  
RA Bishop R.P.; Gobright E.E.I.;  
RL Submitted (APR-1997) to the EMBL/Genbank/DBJ databases.  
CC -!- FUNCTION: ACTS AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES. INDUCES  
CC GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL  
CC CIRCUMSTANCES OR CELL TYPE, BUT BOTH ACTIVITIES ARE INVOLVED IN  
CC TUMOR SUPPRESSION. ACTS IN CELL CYCLE REGULATION, IS A TRANS-  
CC ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION BY  
CC CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF THE  
CC ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES.  
CC APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF  
CC BAX AND BCL-2 ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2  
CC EXPRESSION.  
CC -!- SUBCELLULAR LOCATION: AS AN HOMOTETRAMER (BY SIMILARITY).  
CC -!- SUBCELLULAR LOCATION: Nuclear.  
CC -!- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY  
CC OF TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED  
CC IN MANY TYPES OF CANCER.  
CC -!- SIMILARITY: BELONGS TO THE P53 FAMILY.  
CC  
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CC use by non-profit institutions as long as its content is in no way  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; X81704; CAA57348.1; -  
CC EMBL; D49825; BAA08629.1; -  
CC EMBL; U74486; AAB51214.1; -  
CC HSP; P04637; LYCR.  
CC InterPro: IPR002117; P53.  
CC PRINTS; PR00386; P53SUPPRESSR.  
CC ProDom; PD002681; P53; 1.  
CC PROSITE; PS00348; P53; 1.  
CC Anti-oncogene; DNA-binding; Transcription regulation; Activator;  
CC Nuclear protein; Phosphorylation; Apoptosis.  
CC DOMAIN 1 44 TRANSCRIPTION ACTIVATION (ACIDIC).  
CC FT FT BIND 94 285 BY SIMILARITY.  
CC FT FT DOMAIN 318 349 OLIGOMERIZATION.  
CC FT FT DOMAIN 361 380 BASIC (REPRESSION OF DNA-BINDING).  
CC FT FT DOMAIN 304 316 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).  
CC FT FT MOD\_RES 385 385 PHOSPHORYLATION (BY SIMILARITY).  
CC FT FT CONFLICT 380 380 R -> T (IN REF. 2).  
CC SQ SEQUENCE 386 AA; 43255 MW; 222473F28C548F31 CRC64;  
  
Query Match 22.5%; Score 760.5; DB 1; Length 386;  
Best Local Similarity 44.2%; Pred. No. 7.4e-44;  
Matches 169; Conservative 63; Mismatches 105; Indels 45; Gaps 11;  
  
QY 60 SYMAQFNLLSTWDQMSRAASASYT-----PEHAASVPTHS-PAQAQSSFTFTM 109  
DB 24 NLPENLLSS-----EUSAPVDLLPTDVAWLDECNEAPQMEPSAPAAPPAT---- 76  
  
QY 110 SPAPV-----IPSTNDYDGPGHFEFTQOSTAKSATWYTSPLKLYCQIAKTCPI 161  
DB 77 -PATASWPLSSFPVSKQTPGNYGFRGLQSGTAKSVTCTYSPSLNKLFCOLAKTCPV 135  
  
QY 162 QIKYSTPPPGTATRAMPYKKAETHVDVVKCPNHELGRDFNQGAPASHLIRVEGNN 221  
DB 136 QLWYDSPPPPGCTVRMAIYKLEHTVEVRCPPHRESSDSISG-LAPQHILIRVEGNL 194  
  
QY 222 LSOYVDDPVTGROSVVVPVPPGVGTFTILYNFMCNSSCGVMNRRPILITILEMRD 281  
DB 195 RAEYLDNRNTRFISVVVPVYESPIDSECTIHYNFMCSNCGVMNRRPILITILEDSC 254  
  
QY 282 GOVLGRSFEGRICACPGDRKADHDYHQ-QALNESAANGKAASKRAFKQSPAPVAL 340  
DB 255 GNLLGRNSFEVRCACPGDRRTEENLRKKQSCPEPPPR---STKRALPTNTSSPQ- 310

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|    |  |  |
|----|--|--|
| DR | EMBL; U57306; ARC60146.1; -                                      |  |
| DR | HSSP; P04637; 1YCS.  |  |
| DR | InterPro; IPR002117; P53.  |  |
| DR | Pfam; PF00870; P53; 1.   |  |
| DR | PRINTS; PR00386; P53SUPPRESSR.                                   |  |
| DR | ProDom; PD002681; P53; 1.  |  |
| DR | PROSITE; PS00348; P53; 1.  |  |
| DR | Anti-oncogene; DNA-binding; Transcription regulation; Activator; |  |
| KW | Nuclear protein; Phosphorylation; Apoptosis.                     |  |
| FT | DOMAIN   | 1 47                                       |
| FT | DNA_BIND   | 86 272                                     |
| FT | DOMAIN   | 301 330                                    |
| FT | DOMAIN   | 333 349                                    |
| FT | DOMAIN   | 282 294                                    |
| FT | MOD_RES  | 350 350                                    |
| FT | SEQUENCE   | 351 AA; 390666 MW; BC6153363568BEAL CRC64; |
| SQ |  |  |

Query Match 23.28; Score 752; DB 1; Length 351;  
Best Local Similarity 43.2%; Pred. NO. 2.4e-43;  
Matches 162; Conservative 49; Mismatches 106; Indels 58; Gaps

|    |     |          |          |            |         |          |            |          |                      |                    |
|----|-----|----------|----------|------------|---------|----------|------------|----------|----------------------|--------------------|
| QY | 9   | PDGGTTT  | FEHLWSLS | PESTDYFDLP | QSSRGNN | VGGTDSMD | VPHLEGMTTS | YMAQFNLL | 68                   |                    |
|    |     |          | :        |            | :       |          | :          |          | :                    |                    |
| Db | 8   | PESQSG   | QOELWETV | YPLETISL   | PTV---- | NEPTGS   | WATGDMFLD  | -----    | QDL 53               |                    |
| QY | 69  | SSTQDMQ  | SSRAAS   | PYPPEHA    | SVTHSP  | SYAOPS   | STDTMS     | PAPVIPS  | NTDYPGPHPE 128       |                    |
|    |     |          | :        |            | :       |          | :          |          | :                    |                    |
| Db | 54  | SGTD---- | -----    | DKIFDIP    | -----   | IBFVPT   | NEVNPPTV   | PTVPTD   | PGSYELE 94           |                    |
| QY | 129 | VTFOQS   | TAKSAT   | WYSPLK     | LKLYCOI | ACTCPTQ  | IKVSTP     | PPPGTAIR | AMPVYKKAHVT 188      |                    |
|    |     |          | :        |            | :       |          | :          |          | :                    |                    |
| Db | 95  | LRFOQ    | SGTAKSV  | TSYTS      | ETLUNK  | LYCOLAKT | SPLEVR     | SKPEPKG  | AITRATAYVKKTEHVA 154 |                    |
| QY | 189 | DVVKRC   | NHBLGR   | DFNEG      | OSAPASH | LIRVEGN  | LSQYDD     | PVTGRO   | SVVVPYEPQVGT 248     |                    |
|    |     |          | :        |            | :       |          | :          |          | :                    |                    |
| Db | 155 | DVVRCP   | PHQ----- | NEDS       | VEHRS   | HLIR     | VEGSOLA    | QYFEDPT  | TKQSVTVYEPQPGSE 209  |                    |
| QY | 249 | FTTILY   | NFCN     | SSCVG      | MNRRP   | ILITI    | EMR        | DQGVLR   | RRSEFGRICAC          | PGDRKADSDH 308     |
|    |     |          | :        |            | :       |          | :          |          | :                    |                    |
| Db | 210 | MTTIL    | SU       | MCN        | SCGM    | MNRRP    | ILITITLE   | -TEGLV   | LRRCFEV              | RICACPGDRKTEES 268 |
| QY | 309 | YREQAL   | NESSAK   | GAASKR     | ATFKQ   | SPAPV    | ALGAG      | VKKRRH   | GD-----              | DYYLYQVRGREN 364   |
|    |     |          | :        |            | :       |          | :          |          | :                    |                    |
| Db | 269 | RQKTQ    | PKRKY    | TPNT       | SSSRK   | -----    | KHS        | SGEEDN   | REVFHFVYIGR 313      |                    |
| QY | 365 | FEIM     | KLK      | ESLE       | ME      | 379      |            |          |                      |                    |
|    |     |          | :        |            | :       |          | :          |          | :                    |                    |
| Db | 314 | YEF      | LK       | IND        | GLE     | LE 328   |            |          |                      |                    |
|    |     |          | :        |            | :       |          | :          |          | :                    |                    |

| RESULT 14 |  |                                   |         |
|-----------|--|-----------------------------------|---------|
| P53_CAVPO |  |                                   |         |
| ID        | P53_CAVPO  | STANDARD;                         | PRT;    |
| AC        | Q9WUR6;  |                                   | 391 AA. |
| AD        | 16-OCT-2001  | (Rel. 40, Created)                |         |
| DT        | 16-OCT-2001  | (Rel. 40, Last sequence update)   |         |
| DT        | 16-OCT-2001  | (Rel. 40, Last annotation update) |         |
| DT        | 16-OCT-2001  | (Rel. 40, Last sequence update)   |         |
| DN        | Cellular tumor antigen p53 (tumor suppressor p53). |                                   |         |
| GN        | TP53   |                                   |         |

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Hystriognathii; Caviidae; Cavia.  
OXX NCBI\_TaxID=10141;  
[1] NRN  
SEQUENCE FROM N.A.  
RCR TISSUE=Spleen;  
RX MEDLINE=99285972; PubMed=10331945;

[illegible]

D'erchia A.M., Pesole G., Tullo A., Saccone C., Sbisa E.; "Guinea pig p53 mRNA: identification of new elements in coding and untranslated regions and their functional and evolutionary implications."; Genomics 58:50-64(1999).

- !- FUNCTION: ACTS AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES. INDUCES GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL CIRCUMSTANCES OR CELL TYPE, BUT BOTH ACTIVITIES ARE INVOLVED IN TUMOR SUPPRESSION. ACTS IN CELL CYCLE REGULATION, IS A TRANS-ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION BY CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF THE ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES. APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY SIMULATION OF BAX AND FAS ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2 EXPRESSION.
- !- SUBUNIT: BINDS DNA AS AN HOMOTETRAMER (BY SIMILARITY).
- !- SUBCELLULAR LOCATION: Nuclear.
- !- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY OF TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED IN MANY TYPES OF CANCER.
- !- SIMILARITY: BELONGS TO THE P53 FAMILY.

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|                                |     |     |     |          |     |     |     |                                      |
|--------------------------------|-----|-----|-----|----------|-----|-----|-----|--------------------------------------|
| EMBL; AJ009673; CAB43196.1; -  | 1   | 44  | TTT | DOMAIN   | 1   | 44  | TTT | Nuclear protein; DNA-phosphorylation |
| HSP; P04637; 1YCR              | 100 | 290 | TTT | DNA_BIND | 100 | 290 | TTT | Thymine                              |
| InterPro: IPR002117; P53.      | 323 | 354 | TTT | DOMAIN   | 323 | 354 | TTT | O                                    |
| Pfam: PF00870; P53; 1.         | 366 | 385 | TTT | DOMAIN   | 366 | 385 | TTT | BL                                   |
| PRINTS: PR00386; P33SUPPRESSR. | 309 | 321 | TTT | DOMAIN   | 309 | 321 | TTT | NN                                   |
| ProDom: PD002681; P53; 1.      | 390 | 390 | TTT | MOD_RES  | 390 | 390 | TTT | PI                                   |
| PROSITE: PS00348; P53; 1.      | 391 | AA; | TTT | SEQUENCE | 391 | AA; | TTT | 43287 MW;                            |
| Anti-oncogene; DNA-binding; Tr |     |     |     |          |     |     |     |                                      |

|                       |       |                    |       |             |
|-----------------------|-------|--------------------|-------|-------------|
| Query Match           | 22.2% | Score 750.5;       | DB 1; | Length 391; |
| Best Local Similarity | 43.5% | Pred. No. 3.5e-43; |       |             |

|              |                  |                                |                                   |                                 |
|--------------|------------------|--------------------------------|-----------------------------------|---------------------------------|
| Matches 173; | Conservative 67; | Mismatches 109;                | Indels 49;                        | Gaps 13;                        |
| QY           | 21               | SLBP----                       | DSYTFDLPSSRGNEVVGGTSSMDYFHL       | EGMTTSMVAQFNLLSTWDMSS 77        |
|              |                  |                                |                                   |                                 |
| Db           | 9                | STIEPPLSQTF                    | SDLWKLPPENNVNLS                   | SDSLSPMD--HL-----LLSP--EEVAS 52 |
| QY           | 78               | RAASAPYTP                      | EEAASVPTHSYAPQSFSTFTMTSPAPV-----  | IPSTNDYVPGPHFEV 129             |
|              |                  |                                |                                   |                                 |
| Db           | 53               | WLGE-NPDGDGHVSAAPYSE--         | APTSAGPALYAPAPATSWPLSSSVPS        | HKPTRGSGFEV 109                 |
| QY           | 130              | TQOOSTAKSATWTS                 | PLLKLYCOIAKTCIOIKVSTPPPGTAIRAMPYV | TKAHEHYTD 189                   |
|              |                  |                                |                                   |                                 |
| Db           | 110              | HLKSGTAKSVTCY                  | SPGLNKFQLAKTCPVQWVESPPPGTRV       | RAIAIYKKSQHTE 169               |
| QY           | 190              | VYKRCPNHELGRDFNEGOSAP          | SHALIRVEGNLNLSQYDDPVTGRQSVVVP     | PEPVOVGTEF 249                  |
|              |                  |                                |                                   |                                 |
| Db           | 170              | VYRCPHERCSD-SDG-LAPPQHLIRVEGNL | HAETVDDTRFHSVWVVP                 | PEVSGDC 227                     |
| QY           | 250              | TTILNFMCNSSCVGMNRRPILIIIT      | LEMRDQVILGRSFECRICACPGRDR         | KADEHY 309                      |
|              |                  |                                |                                   |                                 |
| Db           | 228              | THIHYNMCNSSCGMNRPIITIIIT       | EDSSGKLIGRDSFEVRYC                | ACPGRDRTEENF 287                |
| QY           | 310              | REQOAL-NESSAKNGASKAFQSP        | PAYPALGAGVKKRRHGD                 | ETTYLVQVRGRENFEIL 368           |
|              |                  |                                |                                   |                                 |

Db 288 RKKGLCPPTPGN---IKRALPTSSSPQ-----PKKKPLDAEFTLKIRGRKNFEIL 339

QY 369 MKLAKESLELMELVQPLVDYSYRQOQLLRPSHLQPPS 406

Db 340 REINEALEFK-----DAQTEKEGESRPHSSYPKS 369

RESULT 15

PS3\_MESAU STANDARD; PRT; 396. AA.

ID P53\_MESAU

AC Q00366; P97276;

DT 01-DEC-1992 (Rel. 24, Created)

DT 01-DEC-1992 (Rel. 24, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Cellular tumor antigen p53 (tumor suppressor p53).

GN TP53.

OS Mesocricetus auratus (Golden hamster).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;

OC Mesocricetus

OX NCBI\_TaxID=10036;

RN [1]

SEQUENCE FROM N.A.

RP STRAIN-SYRIAN; TISSUE-Kidney;

RC MEDLINE=92210007; PubMed=1555773;

RX Legros Y., McIntyre P., Soussi T.;

RA "The cDNA, cloning and immunological characterization of hamster p53.";

RL Gene 112:247-250(1992).

RN [2]

SEQUENCE FROM N.A.

RA Hou E.W., Wiseman R.;

RL Submitted (APR-1994) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: ACTS AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES. INDUCES GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL CIRCUMSTANCES OR CELL TYPE. BUT BOTH ACTIVITIES ARE INVOLVED IN TUMOR SUPPRESSION. ACTS IN CELL CYCLE REGULATION. IS A TRANS- ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION BY CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF THE ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES. APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF BAX AND FAS ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2 EXPRESSION.

CC -1- SUBUNIT: BINDS DNA AS AN HOMOTETRAMER (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: Nuclear.

CC -1- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY OF TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED IN MANY TYPES OF CANCER.

CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.

CC -----

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CC -----

CC EMBL; M75144; AAA37085.1; .

DR EMBL; U07182; AAB41344.1; .

DR PIR; JH0633; JH0633.

DR HSP; P04637; LYCO.

DR InterPro; IPR002117; P53.

DR Pfam; PF00870; P53; 1.

DR PRINTS; PR00386; P53SUPPRESSR.

DR ProDom; PD002681; P53; 1.

DR PROSITE; PS00348; P53; 1.

DR Anti-oncogene; DNA-binding; Transcription regulation; Activator;

KW Nuclear protein; Phosphorylation; Apoptosis.

FT DOMAIN 1 45

FT DNA\_BIND 105 295

FT DOMAIN 328 359

FT DOMAIN 371 390

FT DOMAIN 314 326

FT BASIC (REPRESSION OF DNA-BINDING).

FT NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).

FT MOD\_RES 395 PHOSPHORYLATION (BY SIMILARITY).

FT CONFLICT 188 G -> S (IN REF. 2).

SQ SEQUENCE 396 AA; 43631 MW; 906EF0256809BE3 CRC64;

Query Match 22.1%; Score 749; DB 1; Length 396;

Best Local Similarity 43.8%; Pred. NO. 4.5e-43;

Matches 165; Conservative 58; Mismatches 104; Indels 50; Gaps 10;

QY 14 TFEHLWSSLEPDSYFDLPQSSRGNNVVGTTSSMDVHFLEGMTTSYMAQFNLLSSTMD 73

Db 18 TFSDLMLKLLPNNVLTLPSS-----DSIEELFLENVA-----GWLEDPGE 59

QY 74 QMSRAASASPYTPEHAASVP---THSPYAQPSSTFDNTPAPV---TPSNTDYPGPHF 127

Db 60 ALOGSAARAAAP--AAEDPVAETPAPVASAPAT-----PWPLSSVPSYKTYGDIYF 112

QY 128 EVTFQOOSTAKSATWYSPLLKLYCQIAKTCPIQIKVSTPPPGTAIRAMPVYKKAHV 187

Db 113 RLGLHSGTAKSVCTYSPSLNKLFCQAKTCVQLWVSTPPPGTVRAMAIYKKLQYM 172

QY 188 TDVVKRCPNHGLGRDFNEGOS--APASHLIRVEGNLSQYVDDPVTGQSVVYPPQVG 246

Db 173 TEVVRCPHHERS---SEGDLAPPQHLIRVEGNMHAETLDDKQTFRHSVVVYEPPEVG 229

QY 247 TEFTIILNFMCSNCCVGGMNRRLPIIIILEMRDGOVLGRSFEGRICACGRDRKADE 306

Db 230 SDCITIHVNYMCSNCCMGMNRRLPIITLEDPSGNLLGRNSFEVRICACGRDRTEE 289

QY 307 DHYREQ---QALNESSAKNGAASKRAFKOSPPAPVAPALGAGVKKRRHGDDETYLQVGR 362

Db 290 KNFQKKGPCPELPKSAKRALPTNTSSPQ-----KRLTLDGEYFTLKIRGQ 338

QY 363 ENFEILMKLKSLELME 379

Db 339 ERFKMFQELNEALELKD 355

Search completed: November 7, 2002, 10:09:04

Job time : 12.0455 secs